

Figure 1

## Stability Study of SAHH

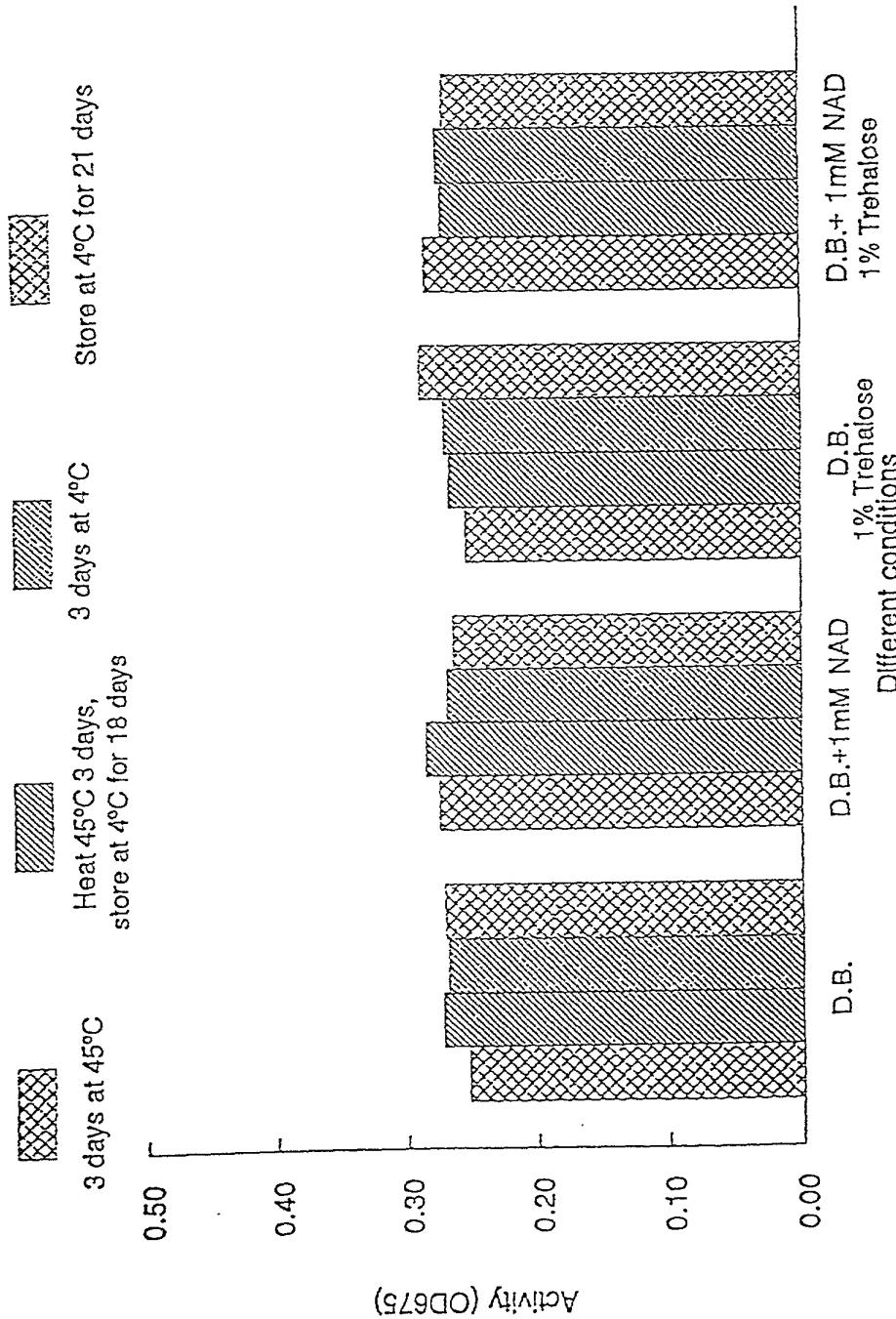


Figure 2

## Screening of SAHH

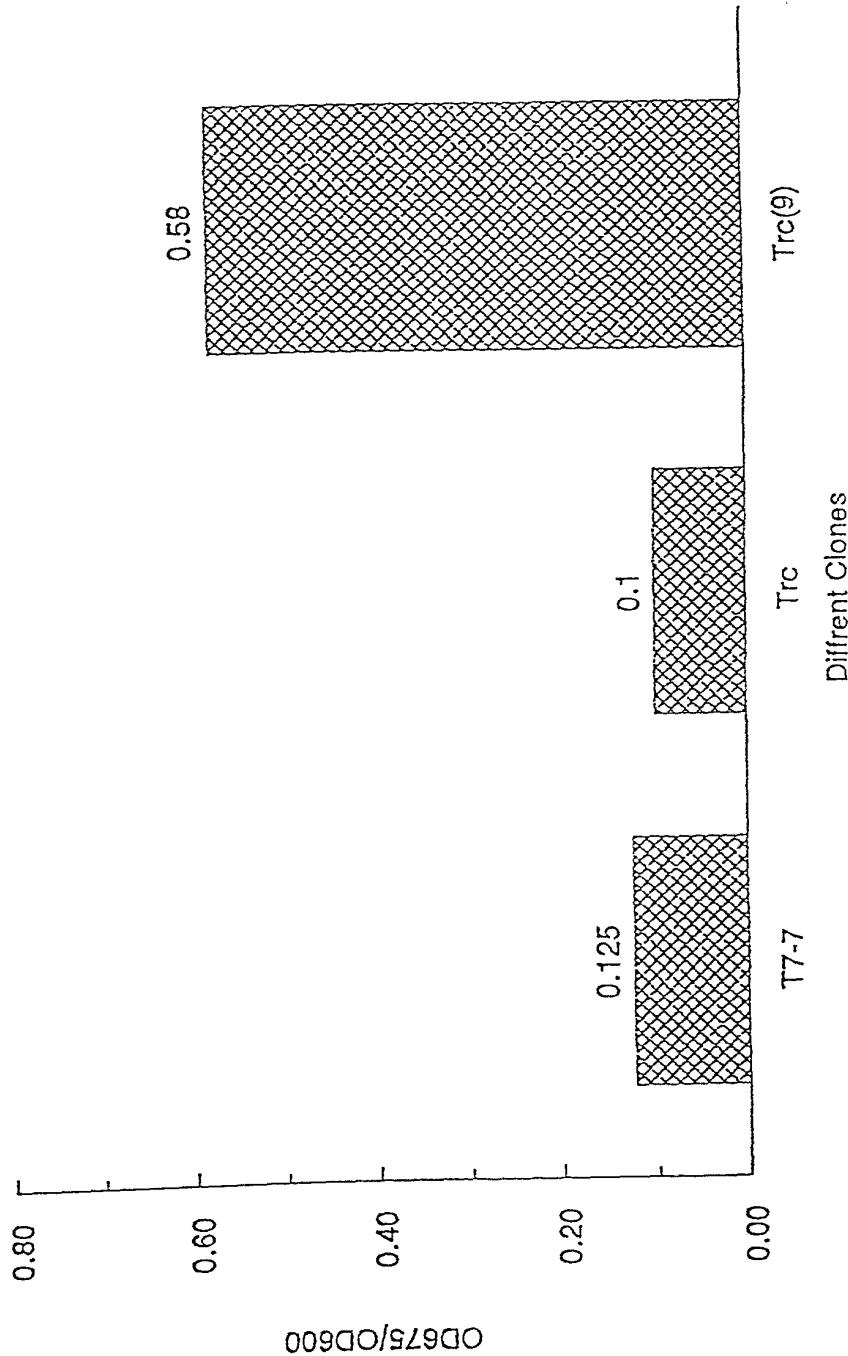


Figure 3

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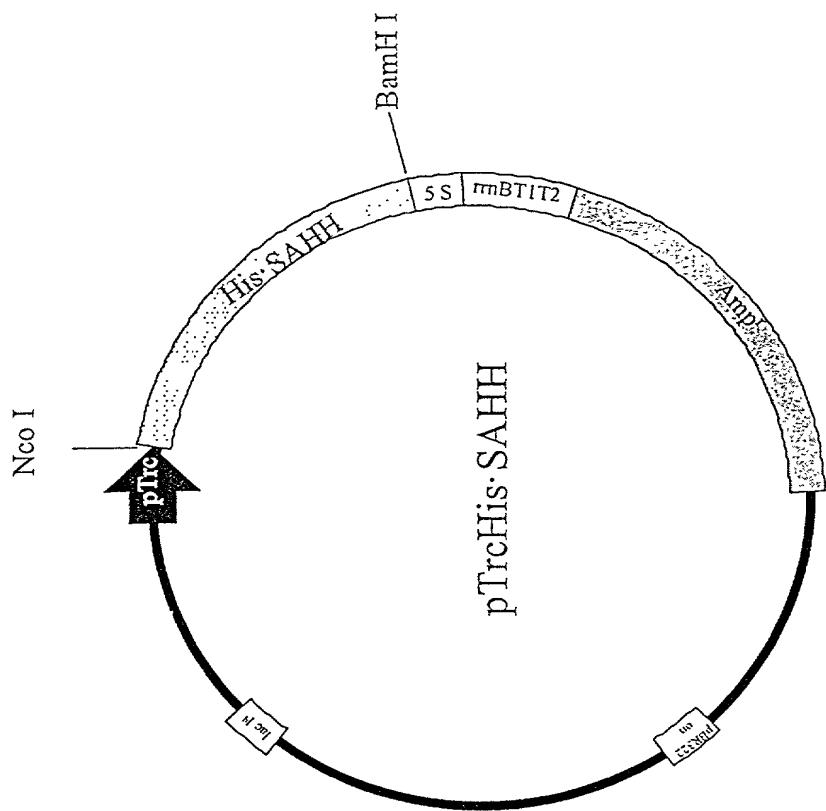


Figure 4

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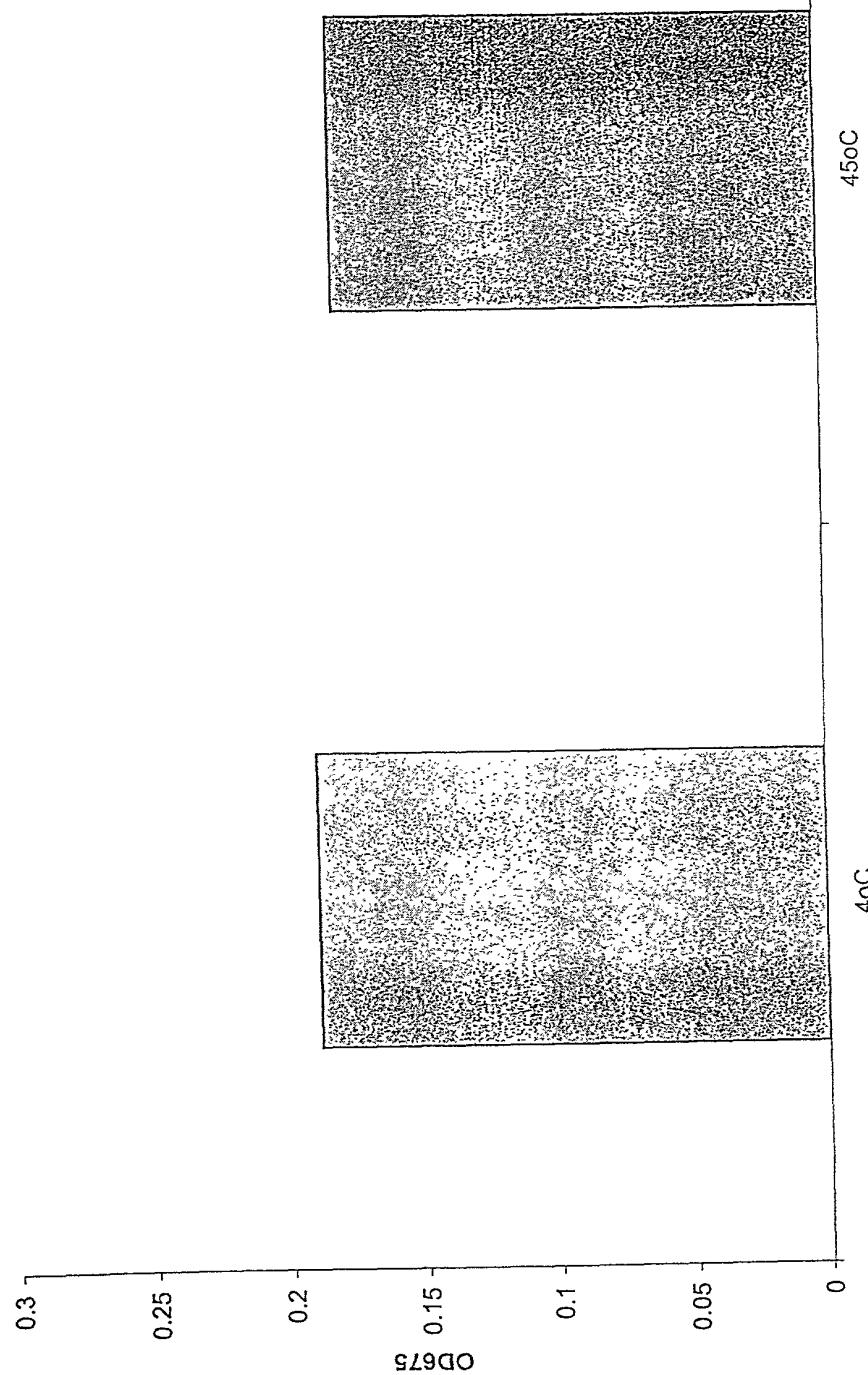


Figure 5

99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

SAHH-wild 291 ATGGCTTGCAAATCACCTGCTGGTGCCTCATTGAGTACAGAATTGCCGACATCAACCTC  
A/C, 71 ATGGCTTGCAAATCACCTACTGGTGCCTCATTGAGTACAGAATTGCCGACATCAACCTC  
\*\*\*\*\*  
SAHH-wild 351 CATGTTCTCGGCCGTAAAGGAACCTACCCCTGCTGAGAAGGAAATGCCAGGTCTTATGGTT  
A/C, 131 CATGTTCTCGGCCGTAAAGGAACCTACCCCTGCTGAGAAGGAAATGCCAGGTCTTATGGTT  
\*\*\*\*\*  
SAHH-wild 411 CTTCGTGAGCGTTATTCCGCTTCTAACGCCATTGAAGGGTGTCAAGAACATCTGGTCCCTC  
A/C, 191 CTTCGTGAGCGTTATTCCGCTTCTAACGCCATTGAAGGGTGTCAAGAACATCTGGTCCCTC  
\*\*\*\*\*  
SAHH-wild 471 CACATGACAGTCCAGACAGCGGTCTTATTGAGACACTCACAGCTCTGGTGCTGATGTC  
A/C, 251 CACATGACAGTCCAGACAGCGGTCTCATCGAGACACTCACAGCTCTGGTGCTGATGTC  
\*\*\*\*\*  
SAHH-wild 531 AGATGGGCTCTGCAAACATCTCTACACAAGATAACAGCCGCTGCTGCTATCGTTGTC  
A/C, 311 AGATGGGCTCTGCAAACATCTCTACACAAGATAACAGCCGCTGCTGCTATCGTTGTC  
\*\*\*\*\*  
SAHH-wild 591 GGCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTCGCCTGGAAGGGCGAA  
A/C, 371 GGCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTCGCCTGGAAGGGCGAA  
\*\*\*\*\*  
SAHH-wild 651 ACACCTCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCAGATGGTCAAGGC  
A/C, 431 ACACCTCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCAGATGGTCAAGGC  
\*\*\*\*\*  
SAHH-wild 711 CCACAGCAGGTGTCGATGATGGTGGTGTACACTCCATCTCCAAGGGCTTCGAA  
A/C, 491 CCACAGCAGGTGTCGATGATGGTGGTGTACACTCCATCTCCAAGGGCTTCGAA  
\*\*\*\*\*  
SAHH-wild 771 TTCGAAACAGCCGGTGTCTCCAGAGCCAACAGAACAGCTGACAACCTCGAATACCGCTGC  
A/C, 551 TTCGAAACAGCCGGTGTCTCCAGAGCCAACAGAACAGCTGACAACCTCGAATACCGCTGC  
\*\*\*\*\*  
SAHH-wild 831 GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGAACAAAGAACACTGGCACACAGTTGCT  
A/C, 611 GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGAACAAAGAACACTGGCACACAGTTGCT  
\*\*\*\*\*  
SAHH-wild 891 GCCGGCATGAACGGTGTTCGAAGAGAACAAACAGGTGTCCACCGCCTCTACAGCTC  
A/C, 671 GCCGGCATGAACGGTGTTCGAAGAGAACAAACAGGTGTCCACCGCCTCTACAGCTC  
\*\*\*\*\*  
SAHH-wild 951 GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC  
A/C, 731 GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC  
\*\*\*\*\*  
SAHH-wild 1011 AAGTCGATAACATCTACGGCTGCCCCACTCCCTTATCGATGGTATCAACCGTGCTTCC  
A/C, 791 AAGTCGATAACATCTACGGCTGCCCCACTCCCTTATCGATGGTATCAACCGTGCTTCC  
\*\*\*\*\*  
SAHH-wild 1071 GATGTCATGATCGCGGCAAGACAGCTCTCGTATGGTTACGGCGATGTCGGGAAGGGC  
A/C, 851 GATGTCATGATCGCGGCAAGACAGCTCTCGTATGGTTACGGCGATGTCGGCAAGGGC  
\*\*\*\*\*  
SAHH-wild 1131 TGCGCTCAATCCCTCCGTGGCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCCTATC  
A/C, 911 TGCGCTCAATCCCTCCGTGGCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCCAATC  
\*\*\*\*\*

Figure 6a

SAHH-wild A/C,	1191 TGCGCTCTCCAGGCTGTACATGGAAGGCATTACAGGTCCGCCATCGAGGAAGTCGTCAAG 971 TGCGCTCTCCAGGCTGCCATGGAAGGCATTACAGGTCCGCCATCGAGGAAGTCGTCAAG *****
SAHH-wild A/C,	1251 GATGTCGATATCTCGTTACATGCACAGGAAACTGCAGATATCATCTCTGTTGACATGATG 1031 GATGTCGATATCTCGTTACATGCACAGGAAACTGCAGATATCATCTCTGTTGACATGATG *****
SAHH-wild A/C,	1311 GCCCAGATGAAGGATAAGGCATTGCGGTAAACATCGGCCACTTCGATAACGAAATTGAT 1091 GCCCAGATGAAGGATAAGGCATTGCGGTAAACATCGGCCACTTCGATAACGAAATTGAT *****
SAHH-wild A/C,	1371 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCAAATCAAGGCCAGAACGAC 1151 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCAAATCAAGGCCAGAACGAC *****
SAHH-wildt A/C,	1431 ATGTGGAATTCCCAGATGGCCACGCTATCCTCCTTCTGCTGAGGGCCGCTTCTTAAC 1211 ATGTGGAATTCCCAGATGGCCACGCTATCCTCCTTCTGCTGAGGGCCGCTTCTTAAC *****
SAHH-wild A/C,	1491 CTTGGTTGCGCTACAGGTCAACCATTTGTTATGTCATGTCATTCAAACACCAGACA 1271 CTTGGCTGCGCTACAGGTCAACCATTTGTTATGTCATGTCATTCAAACACCAGACA *****
SAHH-wild A/C,	1551 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTGAGATGAAGGTTACACACTT 1331 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTGAGAAGAAGGTTACACACTT *****
SAHH-wild A/C,	1611 CGAAGCATCTCGATGAAGAACGAGCTGACTACATCAACGTTCCAGTTGAGGGCCTTACAAG 1391 CGAAGCATCTCGATGAAGAACGAGCTGACTACATCAACGTTCCAGTTGAGGGCCTTACAAG *****
SAHH-wild A/C,	1671 ACAAGCTTACACAGAACGAGCTGACTACATCAACGTTCCAGTTGAGGGCCTTACAAG 1451 ACAAGCTTACACAGAACGAGCTGACTACATCAACGTTCCAGTTGAGGGCCTTACAAG *****
SAHH-wild A/C,	1731 TCTGATGCTTACCGTTATTAA 1511 TCTGATGCTTACCGTTATTAA *****

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65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

SAHH-wild A/C,	782 CGGTGCTGTCCCAGAGCCAACAGAACGCTGACAACCTCGAACATT 682 CGGTGTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTAAC *****
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80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild A/C,	1053 GGTATCAACCGTGCTTCCGA 674 GGCATGAACGGTGTTCGAA ***
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Figure 6b

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87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 564 GATACAGCCGCTGCTG  
A/C, 554 GAAACAGCCGGTGCTG  
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64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 1224 GTCCGCCGCATCGAGGAAGTCGTCAAGGATGTCGATATCTTC  
A/C, 710 GTCCACCGCCTCTACCAGCTCGAGAAGGAGGGCAAACCTCCTC  
\*\*\*\*\* \*\*\* \* \* \*\*\* \*\*\*\*\* \* \* \* \*\*\*

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87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 774 GAAACAGCCGGTGCTG  
A/C, 344 GATACAGCCGCTGCTG  
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Figure 6c